

IN THE SPECIFICATION

Please insert the following section on page 3 between lines 20 and 21 as follows:

BRIEF DESCRIPTION OF DRAWINGS

Fig. 1: Sequence of the human EphA2 receptor (SEQ. ID. NO: 1).

Fig. 2: Induction of specific CTLs by immunization with p58 and p50 peptides.

Fig. 3: Activity of CTL lines for their induces peptides, p58, p550, p61Y, p546 and p883.

Fig. 4: Stimulation of CTL lines with its COS-7 cells expressing EphA2 peptides.

Fig. 5A, B, C: Stimulation of CTL lines with tumor lines detected by TNF- $\alpha$  secretion. Figure 5A shows that the mCTL58 and mCTL550 cells respond to the stimulation with the Caco-2 cells, which express HLA-A\*0201 and EphA2, but respond neither to the DU145 cells, which do not express HLA-A\*0201, nor to the LNCaP cells, which do not express EphA2. Figure 5B shows that the mCTL58 and mCTL550 cells respond to the stimulation with the HIEG, Caco-2, 1355 and SAOS cells, which express large amounts of EphA2, but do not respond to the LNCaP cells, which do not express EphA2. Figure 5C shows that the mCTL61Y, mCTL546 and mCTL883 cells respond to the stimulation of the Caco-2 cells, which express large amounts of EphA2, but do not respond to the LNCaP or DU145 cells, which do not express EphA2 and HLA-A\*0201, respectively.

Figure 6A shows that the human CTLs obtained from CD8<sup>+</sup> cells stimulated, respectively, with the p58 peptide (hCTL58) or the p550 peptide (hCTL550) are activated by the T2 cells loaded with the corresponding peptide, and that no activation by the T2 cells loaded with the irrelevant peptide is observed.

Figure 6B shows a response of the hCTL58 and hCTL550 CTLs with respect to the Caco-2 tumor line (EphA2<sup>+</sup>, HLA-A\*0201<sup>+</sup>), but not with respect to the LNCaP (EphA2<sup>-</sup>, HLA-A\*0201<sup>-</sup>) and DU145 (EphA2<sup>+</sup>, HLA-A\*0201<sup>-</sup>) lines.

Please replace the paragraph at page 4, lines 9-20, with the following rewritten paragraph:

The choice of the peptide sequences capable of constituting epitopes presented by a given MHC I allele can be made, conventionally, by analyzing the peptide sequence of the EphA2 antigen in order to select the peptides which have all or part of the primary anchor motif corresponding to this allele. Various databases which list the known anchor motifs are available: by way of examples, mention will be made of the SYFPEITHI base (~~<http://www.uni-tuebingen.de/uni/kxi/>~~ Hyper Text Transfer Protocol://World Wide Web.uni-tuebingen.de/uni/kxi/; Rammensee et al., Immunogenetics, 50, 213-219, 1999), or the BIMAS base (~~[http://bimas.dcrf.nih.gov/molbio/hla\\_bind](http://bimas.dcrf.nih.gov/molbio/hla_bind)~~ Hyper Text Transfer Protocol://bimas.dcrf.nih.gov/molbio/hla\_bind; Parker et al., J. immunol. 152; 163, 1994).

Please add the following new Abstract on a separate sheet as follows: